



Highly Multiplexed RNA Profiling in Single Cells with Light Microscopy

Abstract:

Physiological processes take place under intricate cellular coordination. The 3D organization of tissue components affects gene expression and is crucial for tissue health. Accurate reconstruction of transcriptomic information of individual cells from intact tissue samples has been a technical challenge. While in the Zhuang Group at Harvard University, Kok Hao co-developed Multiplexed Error-Robust Fluorescence In Situ Hybridization (MERFISH), a method that can spatially image hundreds to thousands of RNA species at the subcellular level (Science 348, aaa6090). Spatial transcriptome analyses promises to transform our understanding in many areas of biology, such as the consequences of cellular heterogeneity, sub-cellular localization of transcripts, and organization of cell types in complex tissues.

Date:

22 Nov 2018 (Thursday)

Venue:

Amphitheatre, Level 2 Duke-NUS Medical School 8, College Road, Singapore 169857

Time:

12pm - 1pm

Host:

Patrick Tan MD, PhD

Professor Programme in Cancer & Stem Cell Biology Duke-NUS Medical School Singapore

No registration is required. All are welcome. Any enquiries, please contact:

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Speaker: Dr.CHEN Kok Hao

GIS Fellow, Genome Institute of Singapore

Kok Hao is a GIS fellow and AXA postdoctoral fellow at the Genome Institute of Singapore. He received his B.S. in chemical engineering from the University of Illinois at Urbana Champaign. He completed his Ph.D. in chemistry and chemical biology from Harvard University, where he worked on developing microscopy techniques and applied them to system biology at the single cell and single molecule level. His current research interest is in the development of spatial transcriptomics technologies.